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## SEQUENCE LISTING

TECH CENTER 1600/2900

<10> Kaufman, Randal J.  
Tirasophon, Witoon  
Welihinda, Ajith A.

<120> Irelp, A NOVEL MAMMALIAN PROTEIN AND GENE ENCODING SAME

<130> UMV-1584

<140> US 09/357,273

<141> 1999-07-20

<150> US 60/093,526

<151> 1998-07-21

<160> 13

<170> PatentIn Ver. 2.0

<210> 1

<211> 3629

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (97)..(3027)

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Met Pro Ala Arg Arg Leu  
1 5

ctg ctg ctg ctg acg ctg ctg ctg ccc ggc ctc ggg att ttt gga agt 162  
Leu-Leu-Leu-Leu-Thr-Leu-Leu-Leu-Pro-Gly-Leu-Gly-Ile-Phe-Gly-Ser-  
10 15 20

acc agc aca gtg acg ctt cct gaa acc ttg ttg ttt gtg tca acg ctg 210  
Thr Ser Thr Val Thr Leu Pro Glu Thr Leu Leu Phe Val Ser Thr Leu  
25 30 35

gat gga agt ttg cat gct gtc agc aag agg aca ggc tca atc aaa tgg 258  
Asp Gly Ser Leu His Ala Val Ser Lys Arg Thr Gly Ser Ile Lys Trp  
40 45 50

act tta aaa gaa gat cca gtc ctg cag gtc cca aca cat gtg gaa gag 306  
Thr Leu Lys Glu Asp Pro Val Leu Gln Val Pro Thr His Val Glu Glu  
55 60 65 70

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Pro Ala Phe Leu Pro Asp Pro Asn Asp Gly Ser Leu Tyr Thr Leu Gly  
75 80 85

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Ser Lys Asn Asn Glu Gly Leu Thr Lys Leu Pro Phe Thr Ile Pro Glu  
90 95 100

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ggt	aaa	aag	cag	gac	atc	tgg	tat	gtt	att	gac	ctc	ctg	acc	gga	gag	498	
Gly	Lys	Lys	Gln	Asp	Ile	Trp	Tyr	Val	Ile	Asp	Leu	Leu	Thr	Gly	Glu		
	120					125				130							
aag	cag	cag	act	ttg	tca	tcg	gcc	ttt	gca	gat	agt	ctc	tgc	cca	tca	546	
Lys	Gln	Gln	Thr	Leu	Ser	Ser	Ala	Phe	Ala	Asp	Ser	Leu	Cys	Pro	Ser		
135					140					145					150		
acc	tct	ctt	ctg	tat	ctt	ggg	cga	aca	gaa	tac	acc	atc	acc	atg	tac	594	
Thr	Ser	Leu	Leu	Tyr	Leu	Gly	Arg	Thr	Glu	Tyr	Thr	Ile	Thr	Met	Tyr		
				155					160					165			
gac	acc	aaa	acc	cga	gag	ctc	cgg	tgg	aat	gcc	acc	tac	ttt	gac	tat	642	
Asp	Thr	Lys	Thr	Arg	Glu	Leu	Arg	Trp	Asn	Ala	Thr	Tyr	Phe	Asp	Tyr		
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gcg	gcc	tca	ctg	cct	gag	gac	gaa	ggg	gac	tac	aag	atg	tcc	cac	ttt	690	
Ala	Ala	Ser	Leu	Pro	Glu	Asp	Glu	Gly	Asp	Tyr	Lys	Met	Ser	His	Phe		
		185					190					195					
gtg	tcc	aat	ggt	gat	ggg	ctg	gtg	gtg	act	gtg	gac	agt	gaa	tct	ggg	738	
Val	Ser	Asn	Gly	Asp	Gly	Leu	Val	Val	Thr	Val	Asp	Ser	Glu	Ser	Gly		
	200					205					210						
gac	gtc	ctg	tgg	atc	caa	aac	tac	gcc	tcc	cct	gtg	gtg	gcc	ttt	tat	786	
Asp	Val	Leu	Trp	Ile	Gln	Asn	Tyr	Ala	Ser	Pro	Val	Val	Ala	Phe	Tyr		
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Val	Trp	Gln	Arg	Glu	Gly	Leu	Arg	Lys	Val	Met	His	Ile	Asn	Val	Ala		
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Val	Glu	Thr	Leu	Arg	Tyr	Leu	Thr	Phe	Met	Ser	Gly	Glu	Val	Gly	Arg		
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Ile	Thr	Lys	Trp	Lys	Tyr	Pro	Phe	Pro	Lys	Glu	Thr	Glu	Ala	Lys	Ser		
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Lys	Leu	Thr	Pro	Thr	Leu	Tyr	Val	Gly	Lys	Tyr	Ser	Thr	Ser	Leu	Tyr		
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gcc	tct	ccc	tca	atg	gta	cac	gag	ggg	gtt	gct	gtc	gtg	ccc	cgc	ggc	1026	
Ala	Ser	Pro	Ser	Met	Val	His	Glu	Gly	Val	Ala	Val	Val	Pro	Arg	Gly		
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agc	aca	ctt	cct	ttg	ctg	gaa	ggg	ccc	cag	act	gat	ggc	gtc	acc	atc	1074	
Ser	Thr	Leu	Pro	Leu	Leu	Glu	Gly	Pro	Gln	Thr	Asp	Gly	Val	Thr	Ile		
				315				320						325			
ggg	gac	aag	ggg	gag	tgt	gtg	atc	acg	ccc	agc	acg	gac	gtc	aag	ttt	1122	
Gly	Asp	Lys	Gly	Glu	Cys	Val	Ile	Thr	Pro	Ser	Thr	Asp	Val	Lys	Phe		
			330					335					340				
gat	ccc	gga	ctc	aaa	agc	aag	aac	aag	ctc	aac	tac	ttg	agg	aat	tac	1170	
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C4  
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atg ctg gag aga ttt ccc aac aat cta ccc aaa cat cgg gaa aat gtg Met Leu Glu Arg Phe Pro Asn Asn Leu Pro Lys His Arg Glu Asn Val 375 380 385 390			1266
att cct gct gat tca gag aaa aag agc ttt gag gaa gtt atc aac ctg Ile Pro Ala Asp Ser Glu Lys Lys Ser Phe Glu Glu Val Ile Asn Leu 395 400 405			1314
gtt gac cag act tca gaa aac gca cct acc acc gtg tct cgg gat gtg Val Asp Gln Thr Ser Glu Asn Ala Pro Thr Thr Val Ser Arg Asp Val 410 415 420			1362
gag gag aag ccc gcc cat gcc cct gcc cgg ccc gag gcc ccc gtg gac Glu Glu Lys Pro Ala His Ala Pro Ala Arg Pro Glu Ala Pro Val Asp 425 430 435			1410
tcc atg ctt aag gac atg gct acc atc atc ctg agc acc ttc ctg ctg Ser Met Leu Lys Asp Met Ala Thr Ile Ile Leu Ser Thr Phe Leu Leu 440 445 450			1458
att ggc tgg gtg gcc ttc atc atc acc tat ccc ctg agc atg cat cag Ile Gly Trp Val Ala Phe Ile Ile Thr Tyr Pro Leu Ser Met His Gln 455 460 465 470			1506
cag cag cag ctc cag cac cag cag ttc cag aag gaa ctg gag aag atc Gln Gln Gln Leu Gln His Gln Gln Phe Gln Lys Glu Leu Glu Lys Ile 475 480 485			1554
cag ctc ctg cag cag cag cag cag cag ctg ccc ttc cac cca cct gga Gln Leu Leu Gln Gln Gln Gln Gln Gln Leu Pro Phe His Pro Pro Gly 490 495 500			1602
gac acg gct cag gac ggc gag ctc ctg gac acg tct ggc ccg tac tca Asp Thr Ala Gln Asp Gly Glu Leu Leu Asp Thr Ser Gly Pro Tyr Ser 505 510 515			1650
gag agc tcg ggc acc agc agc ccc agc acg tcc ccc agg gcc tcc aac Glu Ser Ser Gly Thr Ser Ser Pro Ser Thr Ser Pro Arg Ala Ser Asn 520 525 530			1698
cac tcg ctc tgc tcc ggc agc tct gcc tcc aag gct ggc agc agc ccc His Ser Leu Cys Ser Gly Ser Ser Ala Ser Lys Ala Gly Ser Ser Pro 535 540 545 550			1746
tcc ctg gaa caa gac gat gga gat gag gaa acc agc gtg gtg ata gtt Ser Leu Glu Gln Asp Asp Gly Asp Glu Glu Thr Ser Val Val Ile Val 555 560 565			1794
ggg aaa att tcc ttc tgt ccc aag gat gtc ctg ggc cat gga gct gag Gly Lys Ile Ser Phe Cys Pro Lys Asp Val Leu Gly His Gly Ala Glu 570 575 580			1842
ggc aca att gtg tac cgg ggc atg ttt gac aac cgc gac gtg gcc gtg Gly Thr Ile Val Tyr Arg Gly Met Phe Asp Asn Arg Asp Val Ala Val 585 590 595			1890

C4  
Cont'

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acg gag aag gac cgg caa ttc cag tac att gcc atc gag ctg tgt gca Thr Glu Lys Asp Arg Gln Phe Gln Tyr Ile Ala Ile Glu Leu Cys Ala 635 640 645	2034
gcc acc ctg caa gag tat gtg gag cag aag gac ttt gcg cat ctc ggc Ala Thr Leu Gln Glu Tyr Val Glu Gln Lys Asp Phe Ala His Leu Gly 650 655 660	2082
ctg gag ccc atc acc ttg ctg cag cag acc acc tcg ggc ctg gcc cac Leu Glu Pro Ile Thr Leu Leu Gln Gln Thr Thr Ser Gly Leu Ala His 665 670 675	2130
ctc cac tcc ctc aac atc gtt cac aga gac cta aag cca cac aac atc Leu His Ser Leu Asn Ile Val His Arg Asp Leu Lys Pro His Asn Ile 680 685 690	2178
ctc ata tcc atg ccc aat gca cac ggc aag atc aag gcc atg atc tcc Leu Ile Ser Met Pro Asn Ala His Gly Lys Ile Lys Ala Met Ile Ser 695 700 705 710	2226
gac ttt ggc ctc tgc aag aag ctg gca gtg ggc aga cac agt ttc agc Asp Phe Gly Leu Cys Lys Lys Leu Ala Val Gly Arg His Ser Phe Ser 715 720 725	2274
cgc cga tct ggg gtg cct ggc aca gaa ggc tgg atc gct cca gag atg Arg Arg Ser Gly Val Pro Gly Thr Glu Gly Trp Ile Ala Pro Glu Met 730 735 740	2322
ctg agc gaa gac tgt aag gag aac cct acc tac acg gtg gac atc ttt Leu Ser Glu Asp Cys Lys Glu Asn Pro Thr Tyr Thr Val Asp Ile Phe 745 750 755	2370
tct gca ggc tgc gtc ttt tac tac gtg gtc tct gag ggc agc cac cct Ser Ala Gly Cys Val Phe Tyr Tyr Val Val Ser Glu Gly Ser His Pro 760 765 770	2418
ttt ggc aag tcc ctg cag cgg cag gcc aac atc ctc ctg ggt gcc tgc Phe Gly Lys Ser Leu Gln Arg Gln Ala Asn Ile Leu Leu Gly Ala Cys 775 780 785 790	2466
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gaa ttg ata gag aag atg att gcg atg gat cct cag aaa cgc ccc tca Glu Leu Ile Glu Lys Met Ile Ala Met Asp Pro Gln Lys Arg Pro Ser 810 815 820	2562
gcg aac gac gtg ctc aaa cac ccg ttc ttc tgg agc cta gag aag cag Ala Asn Asp Val Leu Lys His Pro Phe Phe Trp Ser Leu Glu Lys Gln 825 830 835	2610

C4  
Cont

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 840 845 850

gat ggc ccg atc gtg aag cag tta gag aga ggc ggg aga gcc gtg gtg 2706  
 Asp Gly Pro Ile Val Lys Gln Leu Glu Arg Gly Gly Arg Ala Val Val  
 855 860 865 870

aag atg gac tgg cgg gag aac atc act gac ccc ctc cag aca gac ctg 2754  
 Lys Met Asp Trp Arg Glu Asn Ile Thr Asp Pro Leu Gln Thr Asp Leu  
 875 880 885

cgt aaa ttc agg acc tat aaa ggt ggt tct gtc aga gat ctc ctc cga 2802  
 Arg Lys Phe Arg Thr Tyr Lys Gly Gly Ser Val Arg Asp Leu Leu Arg  
 890 895 900

gcc atg aga aat aag aag cac cac tac cgg gag ctg cct gca gag gtg 2850  
 Ala Met Arg Asn Lys Lys His His Tyr Arg Glu Leu Pro Ala Glu Val  
 905 910 915

cgg gag acg ctg ggg acc ctc ccc gac gac ttc gtg tgc tac ttc acg 2898  
 Arg Glu Thr Leu Gly Thr Leu Pro Asp Asp Phe Val Cys Tyr Phe Thr  
 920 925 930

tct cgc ttc ccc cac ctc ctc gca cac acc tac cgg gcc atg gag ctg 2946  
 Ser Arg Phe Pro His Leu Leu Ala His Thr Tyr Arg Ala Met Glu Leu  
 935 940 945 950

tgc agc cac gag aga ctc ttc cag ccc tac tac ttc cac gag ccc cca 2994  
 Cys Ser His Glu Arg Leu Phe Gln Pro Tyr Tyr Phe His Glu Pro Pro  
 955 960 965

gag ccc cag ccc cca gtg act cca gac gcc ctc tgagcgaggg cgccccctct 3047  
 Glu Pro Gln Pro Pro Val Thr Pro Asp Ala Leu  
 970 975

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ccggctttgc agggagacca ggcttcccaa accaagtgcc ttgagctgcc tgctctgcag 3167

cccacagagg acagtgtctga cccaggaag tgggagaagt ggccccctcgt gacctacagg 3227

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 Leu Phe Val Ser Thr Leu Asp Gly Ser Leu His Ala Val Ser Lys Arg  
 35 40 45  
 Thr Gly Ser Ile Lys Trp Thr Leu Lys Glu Asp Pro Val Leu Gln Val  
 50 55 60  
 Pro Thr His Val Glu Glu Pro Ala Phe Leu Pro Asp Pro Asn Asp Gly  
 65 70 75 80  
 Ser Leu Tyr Thr Leu Gly Ser Lys Asn Asn Glu Gly Leu Thr Lys Leu  
 85 90 95  
 Pro Phe Thr Ile Pro Glu Leu Val Gln Ala Ser Pro Cys Arg Ser Ser  
 100 105 110  
 Asp Gly Ile Leu Tyr Met Gly Lys Lys Gln Asp Ile Trp Tyr Val Ile  
 115 120 125  
 Asp Leu Leu Thr Gly Glu Lys Gln Gln Thr Leu Ser Ser Ala Phe Ala  
 130 135 140  
 Asp Ser Leu Cys Pro Ser Thr Ser Leu Leu Tyr Leu Gly Arg Thr Glu  
 145 150 155 160  
 Tyr Thr Ile Thr Met Tyr Asp Thr Lys Thr Arg Glu Leu Arg Trp Asn  
 165 170 175  
 Ala Thr Tyr Phe Asp Tyr Ala Ala Ser Leu Pro Glu Asp Glu Gly Asp  
 180 185 190

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Tyr Lys Met Ser His Phe Val Ser Asn Gly Asp Gly Leu Val Val Thr  
 195 200 205  
 Val Asp Ser Glu Ser Gly Asp Val Leu Trp Ile Gln Asn Tyr Ala Ser  
 210 215 220  
 Pro Val Val Ala Phe Tyr Val Trp Gln Arg Glu Gly Leu Arg Lys Val  
 225 230 235 240  
 Met His Ile Asn Val Ala Val Glu Thr Leu Arg Tyr Leu Thr Phe Met  
 245 250 255  
 Ser Gly Glu Val Gly Arg Ile Thr Lys Trp Lys Tyr Pro Phe Pro Lys  
 260 265 270  
 Glu Thr Glu Ala Lys Ser Lys Leu Thr Pro Thr Leu Tyr Val Gly Lys  
 275 280 285  
 Tyr Ser Thr Ser Leu Tyr Ala Ser Pro Ser Met Val His Glu Gly Val  
 290 295 300  
 Ala Val Val Pro Arg Gly Ser Thr Leu Pro Leu Leu Glu Gly Pro Gln

C4  
 Cont.

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Thr	Asp	Gly	Val	Thr	Ile	Gly	Asp	Lys	Gly	Glu	Cys	Val	Ile	Thr	Pro	
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Ser	Thr	Asp	Val	Lys	Phe	Asp	Pro	Gly	Leu	Lys	Ser	Lys	Asn	Lys	Leu	
				340					345					350		
Asn	Tyr	Leu	Arg	Asn	Tyr	Trp	Leu	Leu	Ile	Gly	His	His	Glu	Thr	Pro	
				355					360					365		
Leu	Ser	Ala	Ser	Thr	Lys	Met	Leu	Glu	Arg	Phe	Pro	Asn	Asn	Leu	Pro	
				370					375					380		
Lys	His	Arg	Glu	Asn	Val	Ile	Pro	Ala	Asp	Ser	Glu	Lys	Lys	Ser	Phe	
385				390					395					400		
Glu	Glu	Val	Ile	Asn	Leu	Val	Asp	Gln	Thr	Ser	Glu	Asn	Ala	Pro	Thr	
				405					410					415		
Thr	Val	Ser	Arg	Asp	Val	Glu	Glu	Lys	Pro	Ala	His	Ala	Pro	Ala	Arg	
				420					425					430		
Pro	Glu	Ala	Pro	Val	Asp	Ser	Met	Leu	Lys	Asp	Met	Ala	Thr	Ile	Ile	
				435					440					445		
Leu	Ser	Thr	Phe	Leu	Leu	Ile	Gly	Trp	Val	Ala	Phe	Ile	Ile	Thr	Tyr	
				450					455					460		
Pro	Leu	Ser	Met	His	Gln	Gln	Gln	Gln	Leu	Gln	His	Gln	Gln	Phe	Gln	
465				470					475					480		
Lys	Glu	Leu	Glu	Lys	Ile	Gln	Leu	Leu	Gln	Gln	Gln	Gln	Gln	Gln	Leu	
				485					490					495		
Pro	Phe	His	Pro	Pro	Gly	Asp	Thr	Ala	Gln	Asp	Gly	Glu	Leu	Leu	Asp	
				500					505					510		

Thr	Ser	Gly 515	Pro	Tyr	Ser	Glu	Ser 520	Ser	Gly	Thr	Ser	Ser 525	Pro	Ser	Thr
Ser	Pro 530	Arg	Ala	Ser	Asn	His 535	Ser	Leu	Cys	Ser	Gly 540	Ser	Ser ,	Ala	Ser
Lys 545	Ala	Gly	Ser	Ser	Pro 550	Ser	Leu	Glu	Gln	Asp 555	Asp	Gly	Asp	Glu	Glu 560
Thr	Ser	Val	Val	Ile 565	Val	Gly	Lys	Ile	Ser 570	Phe	Cys	Pro	Lys	Asp 575	Val
Leu	Gly	His	Gly 580	Ala	Glu	Gly	Thr	Ile 585	Val	Tyr	Arg	Gly	Met 590	Phe	Asp
Asn	Arg	Asp 595	Val	Ala	Val	Lys	Arg 600	Ile	Leu	Pro	Glu	Cys 605	Phe	Ser	Phe
Ala	Asp 610	Arg	Glu	Val	Gln	Leu 615	Leu	Arg	Glu	Ser	Asp 620	Glu	His	Pro	Asn
Val 625	Ile	Arg	Tyr	Phe	Cys 630	Thr	Glu	Lys	Asp	Arg 635	Gln	Phe	Gln	Tyr	Ile 640

C<sup>4</sup>  
Conf.

Ala Ile Glu Leu Cys Ala Ala Thr Leu Gln Glu Tyr Val Glu Gln Lys  
 645 650 655  
 Asp Phe Ala His Leu Gly Leu Glu Pro Ile Thr Leu Leu Gln Gln Thr  
 660 665 670  
 Thr Ser Gly Leu Ala His Leu His Ser Leu Asn Ile Val His Arg Asp  
 675 680 685  
 Leu Lys Pro His Asn Ile Leu Ile Ser Met Pro Asn Ala His Gly Lys  
 690 695 700  
 Ile Lys Ala Met Ile Ser Asp Phe Gly Leu Cys Lys Lys Leu Ala Val  
 705 710 715 720  
 Gly Arg His Ser Phe Ser Arg Arg Ser Gly Val Pro Gly Thr Glu Gly  
 725 730 735  
 Trp Ile Ala Pro Glu Met Leu Ser Glu Asp Cys Lys Glu Asn Pro Thr  
 740 745 750  
 Tyr Thr Val Asp Ile Phe Ser Ala Gly Cys Val Phe Tyr Tyr Val Val  
 755 760 765  
 Ser Glu Gly Ser His Pro Phe Gly Lys Ser Leu Gln Arg Gln Ala Asn  
 770 775 780  
 Ile Leu Leu Gly Ala Cys Ser Leu Asp Cys Leu His Pro Glu Lys His  
 785 790 795 800  
 Glu Asp Val Ile Ala Arg Glu Leu Ile Glu Lys Met Ile Ala Met Asp  
 805 810 815  
 Pro Gln Lys Arg Pro Ser Ala Asn Asp Val Leu Lys His Pro Phe Phe  
 820 825 830  
 Trp Ser Leu Glu Lys Gln Leu Gln Phe Phe Gln Asp Val Ser Asp Arg  
 835 840 845  
 Ile Glu Lys Glu Ser Leu Asp Gly Pro Ile Val Lys Gln Leu Glu Arg  
 850 855 860  
 Gly Gly Arg Ala Val Val Lys Met Asp Trp Arg Glu Asn Ile Thr Asp  
 865 870 875 880  
 Pro Leu Gln Thr Asp Leu Arg Lys Phe Arg Thr Tyr Lys Gly Gly Ser  
 885 890 895  
 Val Arg Asp Leu Leu Arg Ala Met Arg Asn Lys Lys His His Tyr Arg  
 900 905 910  
 Glu Leu Pro Ala Glu Val Arg Glu Thr Leu Gly Thr Leu Pro Asp Asp  
 915 920 925  
 Phe Val Cys Tyr Phe Thr Ser Arg Phe Pro His Leu Leu Ala His Thr  
 930 935 940  
 Tyr Arg Ala Met Glu Leu Cys Ser His Glu Arg Leu Phe Gln Pro Tyr  
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C4  
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Tyr Phe His Glu Pro Pro Glu Pro Gln Pro Pro Val Thr Pro Asp Ala  
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Leu

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<211> 983

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<213> Caenorhabditis elegans

<400> 3

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Ser Ile Gly Asp Asp Glu Glu Lys Thr Ser Ser Thr Ile Leu Val Ser  
 35 40 45

Thr Ile Asp Gly Arg Leu Arg Ala Leu Asp Ser Glu Thr Gly Glu Ile  
 50 55 60

Lys Trp Thr Leu Gln Glu Glu Pro Val Leu Arg Ser Pro Ser Ala Val  
 65 70 75 80

Lys Gln Gly Phe Thr Phe Leu Pro Asn Pro Leu Asp Gly Ser Leu Tyr  
 85 90 95

Val Leu Lys Asn Ser Ser Leu Lys Lys Leu Pro Phe Asn Ile Pro Gln  
 100 105 110

Leu Val His Ala Ser Pro Cys Lys Gly Asn Asp Gly Ile Leu Tyr Ala  
 115 120 125

Gly Ser Lys Lys Asp Val Trp Phe Gly Ile Asp Pro Lys Thr Gly Leu  
 130 135 140

Lys Val Glu Tyr Ile Leu Leu Asn Ile Ser Asp Lys Ile Leu Phe Leu  
 145 150 155 160

Gln Val Glu Thr Leu Ser Ser Ala Ser Ala Asp Arg Ile Cys Pro Ala  
 165 170 175

Asn Gln Lys Gln Thr Ile Phe Leu Gly Arg Thr Glu Tyr Arg Val Ser  
 180 185 190

Met Phe Asp Glu Lys Asn Arg Gly Lys Thr Trp Asn Ala Thr Phe Asn  
 195 200 205

Asp Tyr Ser Ala His Leu Leu Pro Glu Val Asn Thr Trp Pro Phe Lys  
 210 215 220

His Tyr Ala Ser Ser Ser His Gly Tyr Ile Leu Thr Phe Asp Arg Glu  
 225 230 235 240

Thr Gly Glu Met Arg Trp Glu Gln Asp Leu Lys Gln Pro Val Val Ala  
 245 250 255

C4  
 Cont.

Leu Tyr Leu Leu Arg Asp Asp Gly Leu His Lys Leu Pro Phe Glu Val  
 260 265 270  
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 290 295 300  
 Thr Ser Leu Thr Asn Gln Phe Phe Pro Ala Leu Phe Val Gly Glu Ser  
 305 310 315 320  
 Ser Phe Gly Leu Tyr Ala Ile Glu Ala Leu Val Asp His Gln Thr Ile  
 325 330 335  
 Thr Tyr Ser Pro Lys Leu Leu Gly Pro Pro Leu Leu Glu Gly Pro Ala  
 340 345 350  
 Pro Ile Ala Leu Thr Glu Met Glu Lys Glu Glu Tyr Leu Pro Pro Arg  
 355 360 365  
 Arg Pro Ile Ile Arg Asn Ile Pro Pro Ser Ile Thr His Lys Thr Ser  
 370 375 380  
 Asp Gly Glu Tyr Leu Leu Leu Gly Tyr His Asp Arg Pro Met Met Thr  
 385 390 395 400  
 Met Ala Thr Ile Ile Pro Thr Arg Tyr Pro Val Pro Gly Pro His Lys  
 405 410 415  
 Ala Ile Gly Ser Thr Ile Glu Arg Pro Pro Pro Gln Leu Leu Gly Pro  
 420 425 430  
 Val Glu Pro Gln Lys His Glu Asp Thr Ser Phe Ile Leu Leu Leu Leu  
 435 440 445  
 Asn Asn His Pro Ile Pro Phe Tyr Ala Thr Leu Val Thr Met Phe Ala  
 450 455 460

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C4  
 Cont

Leu Leu Leu Thr Val Ile Trp Gln Cys Gly Arg Gln Trp Asp Gln Gln  
 465 470 475 480  
 Lys Ser Thr Ser Arg Met Asp Ser Phe Glu Ile Val Asn Asn Pro Gly  
 485 490 495  
 Glu Ser Arg Ser Ala Gln Thr Ser Lys Gln Ser Asn Arg Gly Ser Phe  
 500 505 510  
 Gly Trp Ala Asn Arg Lys Ile Glu Ile Pro Glu Gly Trp Met Ala Val  
 515 520 525  
 Gly Ser Lys Leu Met Tyr Ser Pro Ser Asp Ile Leu Gly Thr Gly Cys  
 530 535 540  
 Glu Gly Thr Val Val Tyr Arg Gly Thr Phe Asp Gly Arg Glu Val Ala  
 545 550 555 560  
 Val Lys Arg Val Val Ser Glu Phe Val Lys Phe Ala His Arg Glu Ala  
 565 570 575  
 Asp Leu Leu Arg Glu Ser Asp Thr His Pro His Val Ile Arg Tyr Phe



Cys Ser Gly Glu Ala Val Phe Lys Arg Tyr Tyr Ser Asp Asp Val Arg  
 915 920 925

Ala Arg Met Tyr Pro Ile Val Glu Glu Glu Glu Arg Val Arg Lys Lys  
 930 935 940

Ile Lys Glu Glu Met Ala Asn Glu Val Trp Ala Arg Ala Pro Lys Pro  
 945 950 955 960

Val Glu Gln Arg Thr Pro Leu Lys Leu Asp Lys Arg Asn Ile Lys Lys  
 965 970 975

Lys Ser Asn Pro Asn Thr Asp  
 980

&lt;210&gt; 4

&lt;211&gt; 443

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 4

Leu Val Val Ser Cys Lys Ile Leu Gly Tyr Gly Ser Ser Gly Thr Val  
 1 5 10 15

Val Phe Gln Gly Ser Phe Gln Gly Arg Pro Val Ala Val Lys Arg Met  
 20 25 30

Leu Ile Asp Phe Cys Asp Ile Ala Leu Met Glu Ile Lys Leu Leu Thr  
 35 40 45

Glu Ser Asp Asp His Pro Asn Val Ile Arg Tyr Tyr Cys Ser Glu Thr  
 50 55 60

Thr Asp Arg Phe Leu Tyr Ile Ala Leu Glu Leu Cys Asn Leu Asn Leu  
 65 70 75 80

---

Gln Asp Leu Val Glu Ser Lys Asn Val Ser Asp Glu Asn Leu Lys Leu  
 85 90 95

Gln Lys Glu Tyr Asn Pro Ile Ser Leu Leu Arg Gln Ile Ala Ser Gly  
 100 105 110

Val Ala His Leu His Ser Leu Lys Ile Ile His Arg Asp Leu Lys Pro  
 115 120 125

Gln Asn Ile Leu Val Ser Thr Ser Ser Arg Phe Thr Ala Asp Gln Gln  
 130 135 140

Thr Gly Ala Glu Asn Leu Arg Ile Leu Ile Ser Asp Phe Gly Leu Cys  
 145 150 155 160

Lys Lys Leu Asp Ser Gly Gln Ser Ser Phe Arg Thr Asn Leu Asn Asn  
 165 170 175

Pro Ser Gly Thr Ser Gly Trp Arg Ala Pro Glu Leu Leu Glu Glu Ser  
 180 185 190

Asn Asn Leu Gln Cys Gln Val Glu Thr Glu His Ser Ser Ser Arg His  
 195 200 205

C4  
 Cont

Thr Val Val Ser Ser Asp Ser Phe Tyr Asp Pro Phe Thr Lys Arg Arg  
 210 215 220  
 Leu Thr Arg Ser Ile Asp Ile Phe Ser Met Gly Cys Val Phe Tyr Tyr  
 225 230 235 240  
 Ile Leu Ser Lys Gly Lys His Pro Phe Gly Asp Lys Tyr Ser Arg Glu  
 245 250 255  
 Ser Asn Ile Ile Arg Gly Ile Phe Ser Leu Asp Glu Met Lys Cys Leu  
 260 265 270  
 His Asp Arg Ser Leu Ile Ala Glu Ala Thr Asp Leu Ile Ser Gln Met  
 275 280 285  
 Ile Asp His Asp Pro Leu Lys Arg Pro Thr Ala Met Lys Val Leu Arg  
 290 295 300  
 His Pro Leu Phe Trp Pro Lys Ser Lys Lys Leu Glu Phe Leu Leu Lys  
 305 310 315 320  
 Val Ser Asp Arg Leu Glu Ile Glu Asn Arg Asp Pro Pro Ser Ala Leu  
 325 330 335  
 Leu Met Lys Phe Asp Ala Gly Ser Asp Phe Val Ile Pro Ser Gly Asp  
 340 345 350  
 Trp Thr Val Lys Phe Asp Lys Thr Phe Met Asp Asn Leu Glu Arg Tyr  
 355 360 365  
 Arg Lys Tyr His Ser Ser Lys Leu Met Asp Leu Leu Arg Ala Leu Arg  
 370 375 380  
 Asn Lys Tyr His His Phe Met Asp Leu Pro Glu Asp Ile Ala Glu Leu  
 385 390 395 400  
~~Met Gly Pro Val Pro Asp Gly Phe Tyr Asp Tyr Phe Thr Lys Arg Phe~~  
~~405 410 415~~  
 Pro Asn Leu Leu Ile Gly Val Tyr Met Ile Val Lys Glu Asn Leu Ser  
 420 425 430  
 Asp Asp Gln Ile Leu Arg Glu Phe Leu Tyr Ser  
 435 440

C4  
Cont  
 <210> 5

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 5

Ile Ser Asp Phe Gly Leu Cys Lys

1

5

<210> 6

<211> 9  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 6  
cgccatgcc

9

<210> 7  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> misc\_feature  
<222> 1  
<223> N may be Thymine or Cytosine

<220>  
<221> misc\_feature  
<222> 4,9,13,16  
<223> N may be Adenine or Guanine

<220>  
<221> misc\_feature  
<222> 7,10,19,22  
<223> N may be any nucleotide

<220>  
<221> misc\_feature  
<222> 21  
<223> N may be Adenine or Thymine

<220>  
~~<223> Description of Artificial Sequence: Primer~~

<400> 7  
nttncntntnn ccnaantcng nnat

24

<210> 8  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 8  
Ile Ser Asp Phe Gly Leu Cys Lys  
1 5

<210> 9  
<211> 28  
<212> DNA  
<213> Artificial Sequence

C4  
Cont

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Primer

&lt;400&gt; 9

gctctagaac catgccggcc cggcggct

28

&lt;210&gt; 10

&lt;211&gt; 21

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Primer

&lt;400&gt; 10

aggctgccat cattaggatc t

21

&lt;210&gt; 11

&lt;211&gt; 23

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Primer

&lt;400&gt; 11

cattgatgtg catcaccttc ctc

23

&lt;210&gt; 12

&lt;211&gt; 29

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Primer

&lt;400&gt; 12

cggaattcat cacctatccc ctgagcatg

29

&lt;210&gt; 13

&lt;211&gt; 28

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Primer

&lt;400&gt; 13

cggaattctc agagggcgtc tggagtca

28

C4  
Cont